

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 24, 2002, 20:51:21 ; Search time 11.84 Seconds
(Without alignments) 212.565 Million cell updates/sec

Title: US-09-664-326-23
Perfect score: 368

Sequence: 1 LTYTDCETSGNLCICGSGN.....PKQSHNDGDFEIEPEYLD 65

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	360	97.8	65	1	ITH1_HIRME
2	353	95.9	65	1	ITHF_HIRME
3	352	95.7	65	1	ITHK_HIRME
4	350	95.1	65	1	ITHC_HIRME
5	348	94.6	65	1	ITHD_HIRME
6	348	94.6	65	1	ITHE_HIRME
7	346	94.0	65	1	ITHR_HIRME
8	345	93.8	65	1	ITHG_HIRME
9	345	93.8	65	1	ITHJ_HIRME
10	343	93.2	72	1	ITHI_HIRME
11	333	90.5	72	1	ITH3_HIRME
12	315	85.6	66	1	ITH2_HIRME
13	293	79.7	65	1	ITHA_HIRME
14	249	77.6	63	1	ITHV_HIRMA
15	215	58.4	63	1	ITH6_HIRMA
16	173	47.0	62	1	ITHP_HIRMA
17	90	24.5	17	1	ITHB_HIRME
18	68.5	18.6	1071	1	VATA_YEAST
19	68	18.5	192	1	YADX_RHISN
20	67	18.2	222	1	OS28_PLAGA
21	66.5	18.1	810	1	NEIL_HUMAN
22	66	17.9	2282	1	ZAN_RABIT
23	66	17.9	5376	1	ZAN_MOUSE
24	65.5	17.8	2700	1	ZAN_HUMAN
25	65	17.7	306	1	C181_HUMAN
26	64	17.4	317	1	IBP2_SHEEP
27	63.5	17.3	318	1	GSHB_VIBCH
28	63.5	17.3	474	1	VSM5_TRYBB
29	63.5	17.3	755	1	COMP_RAT
30	63.5	17.3	2703	1	NOTC_DROME
31	63	17.1	80	1	AFP4_RARSA
32	63	17.1	385	1	GUNF_FUSOX
33	62.5	17.0	513	1	AVR2_HUMAN

34	62	16.8	79	1	AFP3_BRANA	Q39313 brassica na
35	62	16.8	79	1	AFP3_RARSA	Q24332 raphanus sa
36	62	16.8	80	1	AFP2_ARATH	O80995 arabidopsis
37	62	16.8	80	1	AFP3_ARATH	O80994 arabidopsis
38	62	16.8	80	1	AFP4_ARATH	Q91123 arabidopsis
39	62	16.8	264	1	SPRC_CABEL	P34714 caenorhabdi
40	62	16.8	4660	1	LRP2_RAT	P98158 rattus norv
41	61.5	16.7	335	1	UPAR_HUMAN	Q03405 homo sapien
42	61.5	16.7	383	1	DNAI_PORCI	O9XCA6 porphyromon
43	61.5	16.7	513	1	AVR2_MOUSE	P27038 mus musculu
44	61.5	16.7	513	1	AVR2_RAT	P38444 rattus norv
45	61.5	16.7	4543	1	LRP1_CHICK	P98157 gallus gall

ALIGNMENTS

RESULT	ID	ITH1_HIRME	STANDARD	PRT	65 AA.
AC	P01050:	ITH1_HIRME			
DT	21-JUL-1986	(Rel. 01, Created)			
DT	21-JUL-1986	(Rel. 01, Last sequence update)			
DT	30-MAY-2000	(Rel. 39, Last annotation update)			
DE	Hirudin variant-1 (Lepirudin).				
OS	Hirudo medicinalis (Medicinal leech).				
OC	Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinae;				
OC	Atrynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.				
OX	NCBI_TaxID=6421;				
RN	[1]				
RP	SEQUENCE.				
RA	Dodd J., Mueller H.-P., Seemuller U., Chang J.-Y.;				
RT	"The complete amino acid sequence of hirudin, a thrombin specific				
RT	inhibitor. Application of colour carboxymethylation."				
RL	FEBS Lett. 165:180-183(1984).				
RN	[2]				
RP	SEQUENCE.				
RA	Petersen T.E., Roberts H.R., Sottrop-Jensen L., Magnusson S.,				
RL	Bagdy D.;				
RL	(In) Feleers H. (eds.):				
RL	Protides of the biological fluids, Proc. 23th colloquium, pp.145-149,				
RN	[3]				
RP	STRUCTURE BY NMR.				
RX	MEDLINE=89274194; PubMed=2567183;				
RA	Folkers P.J.M., Clore G.M., Driscoll P.C., Dodd J., Koehler S.,				
RA	Gronenborn A.M.;				
RT	"Solution structure of recombinant hirudin and the Lys-47-->Glu				
RT	mutant: a nuclear magnetic resonance and hybrid distance				
RL	geometry-dynamical simulated annealing study."				
RL	Biochemistry 28:2601-2617(1989).				
RN	[4]				
RP	STRUCTURE BY NMR OF 1-51.				
RX	MEDLINE=93116062; PubMed=1335515;				
RA	Szyperski T., Guentert P., Stone S.R., Wuehrich K.;				
RT	"Nuclear magnetic resonance solution structure of hirudin(1-51) and				
RT	comparison with corresponding three-dimensional structures determined				
RT	using the complete 65-residue hirudin polypeptide chain."				
RL	J. Mol. Biol. 228:1193-1205(1992).				
CC	-1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE				
CC	INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-				
CC	THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.				
CC	-1- PHARMACEUTICAL: Available under the name Refudan (Boehrst Marion				
CC	Roussel). Used to treat heparin-induced thrombocytopenia (HIT).				
CC	-1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.				
CC	-1- DATABASE: NAME=Refudan; NOTE=Clinical information on Refudan;				
CC	WWW="http://www.refudan.com/"				
DR	PIR: A01289; HOLXH.				
DR	PDB: 2HIR; 15-JAN-90.				
DR	PDB: 4HIR; 15-JAN-90.				
DR	PDB: 5HIR; 15-JAN-90.				
DR	PDB: 6HIR; 15-JAN-90.				
DR	PDB: 1HIC; 31-JAN-94.				

DR PDB; 1HAG; 20-DEC-94.
 DR PDB; 1HAG; 20-DEC-94.
 DR InterPro; IPR000429; Hirudin.
 DR Pfam; PF00713; Hirudin; 1.
 DR PRINTS; PR00777; Hirudin.
 DR ProDom; PD004216; Hirudin; 1.
 KW Serine protease inhibitor; Sulfation; Multigene family;
 KW Pharmacological; 3D-structure.
 FT DISULFID 6 14
 FT DISULFID 16 28
 FT DISULFID 22 39
 FT MOD_RES 63 63
 FT STRAND 5 5
 FT STRAND 9 10
 FT STRAND 11 12
 FT STRAND 15 17
 FT STRAND 18 19
 FT STRAND 20 21
 FT STRAND 24 25
 FT STRAND 26 29
 FT STRAND 38 41
 FT STRAND 45 46
 SQ SEQUENCE 65 AA; 6970 MW; 9085A5876E3DE9FF CRC64;

Query Match 97.8%; Score 360; DB 1; Length 65;
 Best Local Similarity 96.9%; Pred. No. 1,6e-32;
 Matches 63; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LVTDTESGQNLCEGSSNVCQGKNCILGSDGKNCVTEGTPKPSHNDGDFEIP 60
 DB 1 VYTDCTESGQNLCEGSSNVCQGKNCILGSDGKNCVTEGTPKPSHNDGDFEIP 60
 OY 61 EYTLQ 65
 DB 61 EYTLQ 65

RESULT 2
 ITHC_HIRME STANDARD; PRT; 65 AA.
 AC P28503; 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Hirudin IIB.
 OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;
 OC Arynchobdellida; Hirudiniiformes; Hirudinae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90005945; PubMed=2792365;
 RA Scharf M., Engels J., Tripiet D.;
 RT "Primary structures of new 'iso-hirudins'";
 RL FEBS Lett. 255:105-110(1989).
 CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
 INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
 THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
 CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
 DR HSP; P01050; 4HTC.
 DR InterPro; IPR000429; Hirudin.
 DR Pfam; PF00713; Hirudin; 1.
 DR PRINTS; PR00777; Hirudin.
 DR ProDom; PD004216; Hirudin; 1.
 KW Serine protease inhibitor; Sulfation; Multigene family.
 FT DISULFID 6 14
 FT DISULFID 16 28
 FT DISULFID 22 39
 FT MOD_RES 63 63
 FT SEQUENCE 65 AA; 6985 MW; 8774EAE5EA30913 CRC64;

Query Match 95.9%; Score 353; DB 1; Length 65;
 Best Local Similarity 93.8%; Pred. No. 9.1e-32;
 Matches 61; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVTDTESGQNLCEGSSNVCQGKNCILGSDGKNCVTEGTPKPSHNDGDFEIP 60
 DB 1 VYTDCTESGQNLCEGSSNVCQGKNCILGSDGKNCVTEGTPKPSHNDGDFEIP 60
 OY 61 EYTLQ 65
 DB 61 EYTLQ 65
 RESULT 3
 ITHC_HIRME STANDARD; PRT; 65 AA.
 AC P28511; 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Hirudin IIB.
 OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;
 OC Arynchobdellida; Hirudiniiformes; Hirudinae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90005945; PubMed=2792365;
 RA Scharf M., Engels J., Tripiet D.;
 RT "Primary structures of new 'iso-hirudins'";
 RL FEBS Lett. 255:105-110(1989).
 CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
 INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
 THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
 CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
 DR HSP; P01050; 1HAG.
 DR InterPro; IPR000429; Hirudin.
 DR Pfam; PF00713; Hirudin; 1.
 DR PRINTS; PR00777; Hirudin.
 DR ProDom; PD004216; Hirudin; 1.
 KW Serine protease inhibitor; Sulfation; Multigene family.
 FT DISULFID 6 14
 FT DISULFID 16 28
 FT DISULFID 22 39
 FT MOD_RES 63 63
 FT SEQUENCE 65 AA; 6968 MW; 85FD9E1AE3DE9FF CRC64;

Query Match 95.7%; Score 352; DB 1; Length 65;
 Best Local Similarity 93.8%; Pred. No. 1.2e-31;
 Matches 61; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LVTDTESGQNLCEGSSNVCQGKNCILGSDGKNCVTEGTPKPSHNDGDFEIP 60
 DB 1 VYTDCTESGQNLCEGSSNVCQGKNCILGSDGKNCVTEGTPKPSHNDGDFEIP 60
 OY 61 EYTLQ 65
 DB 61 EYTLQ 65
 RESULT 4
 ITHC_HIRME STANDARD; PRT; 65 AA.
 AC P28503; 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Hirudin IIB.
 OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;
 OC Arynchobdellida; Hirudiniiformes; Hirudinae; Hirudo.


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OX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE.
RX MEDLINE=90005945; PubMed=2792365;
RA Scharf M., Engels J., Tripler D.;
RT "Primary structures of new 'iso-hirudins'.";
RL FEBS Lett. 255:105-110(1989).
CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
CC INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
CC THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
DR HSSP: P01050: IHAG.
DR InterPro: IPR000429; Hirudin.
DR Pfam: PF00713; Hirudin; 1.
DR PRINTS: PR00777; HIRUDIN.
DR ProDom: PD004216; Hirudin; 1.
KW Serine protease inhibitor; Sulfation; Multigene family.
FT DISULFID 6 14 BY SIMILARITY.
FT DISULFID 16 28 BY SIMILARITY.
FT DISULFID 22 39 BY SIMILARITY.
FT MOD_RES 63 63 SULFATION (BY SIMILARITY).
SQ SEQUENCE 65 AA; 7028 MW; CA8BR0D72B6449E4 CRC64;

Query Match 94.0%; Score 346; DB 1; Length 65;
Best Local Similarity 90.8%; Pred. No. 5,1e-31;
Matches 59; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 LVYDTESGONCLCEGSNVCQGKNCILGSDGKNCVTEGCTPKPSHNDGDEEIP 60
DB : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 VYTDCTESGDLCEGSNVCQGNKCLIGSDGKNECVTEGCTPKPSHNDGDEEIP 60

OY 61 EEXIQ 65
DB 61 EEXIQ 65

RESULT 8
ITHE_HIRME STANDARD: PRT: 65 AA.
ID ITHE_HIRME
AC P28507;
DR 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DE 01-DEC-1992 (Rel. 24, Last annotation update)
DE Hirudin IIA.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
OC Arynchobdellida; Hirudiniformes; Hirudinae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE.
RX MEDLINE=90005945; PubMed=2792365;
RA Scharf M., Engels J., Tripler D.;
RT "Primary structures of new 'iso-hirudins'.";
RL FEBS Lett. 255:105-110(1989).
CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
CC INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
CC THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
DR HSSP: P01050: IHAG.
DR InterPro: IPR000429; Hirudin.
DR Pfam: PF00713; Hirudin; 1.
DR PRINTS: PR00777; HIRUDIN.
DR ProDom: PD004216; Hirudin; 1.
KW Serine protease inhibitor; Sulfation; Multigene family.
FT DISULFID 6 14 BY SIMILARITY.
FT DISULFID 16 28 BY SIMILARITY.
FT DISULFID 22 39 BY SIMILARITY.
FT MOD_RES 63 63 SULFATION (BY SIMILARITY).
SQ SEQUENCE 65 AA; 7028 MW; 05F6A0B26A3DE9FC CRC64;

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Query Match 93.8%; Score 345; DB 1; Length 65;
Best Local Similarity 92.3%; Pred. No. 6,6e-31;
Matches 60; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 LVYDTESGONCLCEGSNVCQGKNCILGSDGKNCVTEGCTPKPSHNDGDEEIP 60
DB : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 VYTDCTESGONCLCQDSNVCQGKNCILGSDGKNECVTEGCTPKPSHNDGDEEIP 60

OY 61 EEXIQ 65
DB 61 EEXIQ 65

RESULT 10
ITHE_HIRME STANDARD: PRT: 65 AA.
ID ITHE_HIRME
AC P28505;
DR 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DE 01-DEC-1992 (Rel. 24, Last annotation update)
DE Hirudin II.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinae;
OC Arynchobdellida; Hirudiniformes; Hirudinae; Hirudo.

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OX NCBI_TaxID=6421;
RN [1]
RP MEDLINE=90005945; PubMed=2792365;
RA Scharf M., Engels J., Tripier D.;
RL "Primary structures of new 'iso-hirudins'.",
CC FBS Lett. 255:105-110(1989).
CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
CC INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
CC THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
DR HSP: P01050; IHAG.
DR InterPro: IPR000429; Hirudin.
DR Pfam: PF00713; Hirudin; 1.
DR PRINTS: PR00777; HIRUDIN.
DR ProDom: PD004216; Hirudin; 1.
KW Serine protease inhibitor; Sulfation; Multigene family.
FT DISULFID 6 14
FT CHAIN 1
FT DISULFID 16 28
FT DISULFID 22 39
FT MOD_RES 63 63
FT MOD_RES 65 AA; 6987 MW; ABLFEAE55FA69ADC CRC64;
SQ SEQUENCE

Query Match 93.2%; Score 343; DB 1; Length 65;
Best Local Similarity 90.8%; Pred. No. 1,le-30;
Matches 59; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTYDCTESGONLCICSGSNVCGGKNCILGSDGKNCVTEGTPKQSHNDDEEIP 60
DB 1 ITTYDCTESGODLCICGSDVCGKNCILGSGNEENOCVTEGTPKQSHNDDEEIP 60
QY 61 EYIQ 65
DB 61 EYIQ 65

RESULT 11
ID ITH3_HIRME STANDARD; PRT; 72 AA.
AC P09945;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Hirudin variant-2 precursor (Fragment).
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudindae; Hirudinea;
OC Arynchobdellida; Hirudiniformes; Hirudindae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86149219; PubMed=3513162;
RA Harvey R.P., Degryse E., Stefan L., Schamber F., Cazeneuve J.-P.,
RA Courtney M., Tolstoshev P., Lecocq J.-P.;
RT "Cloning and expression of a cDNA coding for the anticoagulant
RT hirudin from the bloodsucking leech, Hirudo medicinalis.",
RL Proc. Natl. Acad. Sci. U.S.A. 83:1084-1086(1986).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MUTANT LYS-54.
RX MEDLINE=90321074; PubMed=2374926;
RA Rydel T.J., Ravichandran K.G., Tulinsky A., Bode W., Huber R.,
RA Rolsch C., Fenton J.W. II;
RT "The structure of a complex of recombinant hirudin and human alpha-
RT thrombin.",
RL Science 249:277-280(1990).
CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
CC INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
CC THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
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CC or send an email to license@isb-sib.ch).

DR EMBL: M12693; AAA29195.1; -;
DR EMBL: A14988; CAA01205.1; -;
DR PIR: A37417; A37417.
DR PDB: 3HTC; 31-JAN-94.
DR PDB: 4HTC; 31-JAN-94.
DR InterPro: IPR000429; Hirudin.
DR Pfam: PF00713; Hirudin; 1.
DR ProDom: PD004216; Hirudin; 1.
KW Serine protease inhibitor; Sulfation; Multigene family; Signal;
KW 3D-structure.
FT NON_TER 1 1
FT SIGNAL <1 7
FT CHAIN 8 72
FT DISULFID 13 21
FT DISULFID 23 35
FT DISULFID 29 46
FT MOD_RES 70 70
SQ SEQUENCE 72 AA; 7571 MW; C6EF2F28E9C45A5B CRC64;

Query Match 90.5%; Score 333; DB 1; Length 72;
Best Local Similarity 87.7%; Pred. No. 1,4e-29;
Matches 57; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 LTYDCTESGONLCICSGSNVCGGKNCILGSDGKNCVTEGTPKQSHNDDEEIP 60
DB 8 ITTYDCTESGONLCICSGSNVCGKNCILGSGNKNCVTEGTPKQSHNDDEEIP 67
QY 61 EYIQ 65
DB 68 EYIQ 72

RESULT 12
ID ITH2_HIRME STANDARD; PRT; 66 AA.
AC P09944;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Hirudin PA.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudindae; Hirudinea;
OC Arynchobdellida; Hirudiniformes; Hirudindae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE.
RX MEDLINE=87026247; PubMed=3768144;
RA Dotz J., Machleidt W., Seemüller U., Maschler R., Fritz H.;
RT "Isolation and characterization of hirudin isoforms and sequence
RT analysis of hirudin PA.",
RL Biol. Chem. Hoppe-Seyler 367:803-811(1986).
CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
CC INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
CC THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
CC PIR: A24350; A24350.
DR HSP: P01050; IHIC.
DR InterPro: IPR000429; Hirudin.
DR Pfam: PF00713; Hirudin; 1.
DR PRINTS: PR00777; HIRUDIN.
DR ProDom: PD004216; Hirudin; 1.
KW Serine protease inhibitor; Sulfation; Multigene family.
FT DISULFID 6 14
FT DISULFID 16 28
FT DISULFID 22 39
FT MOD_RES 64 64
SQ SEQUENCE 66 AA; 7026 MW; FA1B80B7FAFEA317 CRC64;

Query Match 85.6%; Score 315; DB 1; Length 66;
 Best Local Similarity 87.1%; Pred. No. 1.1e-27;
 Matches 54; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 LVTDTESGQNLCEGSGNCGGKNCILGSDGKNCVTEGTPKPSHNDGDFEIP 60
 :|||||
 DB 1 LVTDTESGQNLCEGSGNCGGKNCILGSDGKNCVTEGTPKPSHNDGDFEIP 60
 QY 61 EE 62
 :
 DB 61 ED 62

RESULT 13
 ITHA_HIRME STANDARD; PRT: 65 AA.

AC P28501:
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hirudin I (Fragments).
 OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea.
 OC Arynchobdellida; Hirudiniiformes; Hirudinae; Hirudo.
 OX NCBI_TaxId=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90005945; PubMed=2792365;
 RA Scharf M., Engels J., Tipler D.;
 "Primary structures of new 'iso-hirudins'.";
 FEBS Lett. 255:105-110(1989).
 CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
 INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
 THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
 CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
 CC PIR: S05672; S05672.
 DR HSSP: P01050; IHAG.
 DR InterPro: IPR000429; Hirudin.
 DR Pfam: PF00713; Hirudin; 1.
 DR PRINTS: PR00777; HIRUDIN.
 DR Prodom: PD004216; Hirudin; 1.
 KM Serine protease inhibitor; Sulfation; Multigene family.
 FT DISULFID 6 14 BY SIMILARITY.
 FT DISULFID 16 28 BY SIMILARITY.
 FT DISULFID 22 39 BY SIMILARITY.
 FT MOD.RES 63 63 SULFATION.
 SQ SEQUENCE 65 AA; 7126 MW; B79CSA9D11677AD5 CRC64;

Query Match 79.6%; Score 293; DB 1; Length 65;
 Best Local Similarity 81.5%; Pred. No. 2.6e-25;
 Matches 53; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 LVTDTESGQNLCEGSGNCGGKNCILGSDGKNCVTEGTPKPSHNDGDFEIP 60
 :|||||
 DB 1 LVTDTESGQNLCEGSGNCGGKNCILGSDGKNCVTEGTPKPSHNDGDFEIP 60
 QY 61 EYILO 65
 :
 DB 61 EYILO 65

RESULT 14
 ITHV_HIRMA STANDARD; PRT: 63 AA.

AC P81492:
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Hirudin HVI (Bufudrin).
 OS Hirudinaria manillensis (Buffalo leech).

OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Arynchobdellida; Hirudiniiformes; Hirudinae; Hirudinaria.
 OX NCBI_TaxId=6419;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Head;

RX MEDLINE=94000343; PubMed=8397794;
 RA Electicwala A., Hartwell R., Scawen M.D., Atkinson T.;
 "The complete amino acid sequence of a hirudin variant from the leech
 Hirudinaria manillensis.";
 RT Hirudinaria manillensis.
 RL J. Protein Chem. 12:365-370(1993).
 CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
 INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
 THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
 CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
 CC HSSP: P01050; SHIR.
 DR InterPro: IPR000429; Hirudin.
 DR Pfam: PF00713; Hirudin; 1.
 DR PRINTS: PR00777; HIRUDIN.
 DR Prodom: PD004216; Hirudin; 1.
 KM Serine protease inhibitor; Multigene family.
 FT DISULFID 6 14 BY SIMILARITY.
 FT DISULFID 16 28 BY SIMILARITY.
 FT DISULFID 22 37 BY SIMILARITY.
 SQ SEQUENCE 63 AA; 6699 MW; 8BC2828B85C51BED CRC64;

Query Match 67.7%; Score 249; DB 1; Length 63;
 Best Local Similarity 67.7%; Pred. No. 1.4e-20;
 Matches 44; Conservative 8; Mismatches 11; Indels 2; Gaps 1;

QY 1 LVTDTESGQNLCEGSGNCGGKNCILGSDGKNCVTEGTPKPSHNDGDFEIP 60
 :|||||
 DB 1 VAYTDTESGQNLCEGSGNCGGKNCILGSDGKNCVTEGTPKPSHNDGDFEIP 58
 QY 61 EYILO 65
 :
 DB 59 DEXIK 63

RESULT 15
 ITH6_HIRMA STANDARD; PRT: 63 AA.

AC P28512:
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hirudin P6.
 OS Hirudinaria manillensis (Buffalo leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Arynchobdellida; Hirudiniiformes; Hirudinae; Hirudinaria.
 OX NCBI_TaxId=6419;
 RN [1]
 RP SEQUENCE, AND STRUCTURE OF CARBOHYDRATE.
 RX MEDLINE=92172851; PubMed=1540584;
 RA Steiner V., Knecht R., Boersen O., Gassmann E., Stone S.R.,
 Raschdorf F., Schlaeppli J.-M., Maschler R.;
 "Primary structure and function of novel O-glycosylated hirudins from
 the leech Hirudinaria manillensis.";
 RT Biochemistry 31:2294-2298(1992).
 CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
 INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
 THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
 CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
 CC PIR: A42207; A42207.
 DR HSSP: P01050; SHIR.
 DR GlycoSuiteDB: P28512; -
 DR InterPro: IPR000429; Hirudin.
 DR Pfam: PF00713; Hirudin; 1.
 DR PRINTS: PR00777; HIRUDIN.
 DR Prodom: PD004216; Hirudin; 1.
 KM Serine protease inhibitor; Sulfation; Glycoprotein;

KW Multigene family.
FT DISULFID 6 14 BY SIMILARITY.
FT DISULFID 16 28 BY SIMILARITY.
FT DISULFID 22 37 BY SIMILARITY.
FT CARBOHYD 43 43 O-LINKED (GALNAC. . .).
FT MOD_RES 61 61 /FTID-CAR_000143.
SQ SEQUENCE 63 AA; 6977 MM; 149A7369CC75A192 CRC64; SUFFATION (BY SIMILARITY).

Query Match 58.4%; Score 215; DB 1; Length 63;
Best Local Similarity 60.9%; Pred. No. 6.5e-17;
Matches 39; Conservative 7; Mismatches 16; Indels 2; Gaps 1;

QY 1 LFTYDCTESGONLCLCEGSNVCGGNGKCIIGSDGKNCQVTEGCTPKKPOSHNDGDFEIP 60
: ||||| :|||:|||| | :| ||||| :|||
Db 1 MRYTACTESGONQICIGNDVCGGRCNGCFDSSGK--CYEGESTRKRPQNEGOHDFDPIP 58
QY 61 EYTL 64
|||
Db 59 EYTL 62

Search completed: June 24, 2002, 20:54:46
Job time: 205 sec

